

FIGURE 1A

SEQ ID NO:10	*** * * * * *	1
SEQ ID NO:18	-----TYCDLRNKNKEQSREVKNN-----FTEPTRQIKNKMSSSNSKTKTPSS	60
SEQ ID NO:21	MAAAMAATTMTVKNNRASLVMDKKNWLLRPVPEVAFPWSSQPESRS-LDFPRRALFASVG	
	MAATMAVTTMTVTRS-----KESWSSLQVPAVAFPWKPRGGKTGGLEFPFRAMFASVG	60
		1
SEQ ID NO:10	* * * * *	
SEQ ID NO:18	LSLCNSKP---QPQEGNMALESQPQKNKYGHGVFGDVYSII-----KEMEIDHH	
SEQ ID NO:21	LSLSHGAPPV--AREHDGKA-RPAD--DVAHQLAAGAGVQKAQKAKKQQLSLRK-	
	LNVCPGVPAGRDPREDDPKVVRAADNCDIAASLAPPPGSRPPGRRGRGSEEEAEGRRH	120
		61
SEQ ID NO:10	* * * * *	
SEQ ID NO:18	NNSTFDFFQFPPIITNFLGSRE--VREFISGALSGAMTKAILAPLETIRTRMVVG-VGSKNI	
SEQ ID NO:21	-----VRKIGNPHLRLVSGAIAGAVSRTFVAPLETIRTTHLMVGSSGADSM	
	EEAAAAGRSEPEEGQGQDRQPAPARLVSGAIAGAVSRTFVAPLETIRTTHLMVGSIGVDSM	180
		121
SEQ ID NO:10	** * * * * * * * * * *	
SEQ ID NO:18	AGSFIEVIEQQGWQGLWAGNMINMLRIVPTQAIELGTFECVKRAMTSLHEKWESNEYPKL	
SEQ ID NO:21	AGVFRWIMRTEGWPGGLFRGNAVNVLRVAPSKAIEHFTYDTAKKYLTP-----EAGEPAKV	
	AGVFQWIMQNEGTGLFRGNAVNVLRVAPSKAIEHFTYDTAKKFLTP-----KGDEPPKI	240
		181
SEQ ID NO:10	* * * * *	
SEQ ID NO:18	QIGPINFNLSLSWISPVAIAGAAAGIASTLVCHPLEVLKDRLLTVSPETYPYPSLGIARNIY	
SEQ ID NO:21	PIP-----TPL-VAGALAGVASTLCTCTYPMELVKTRLTIEKDVDYDNLLHAFVKIV	
	PIP-----TPL-VAGALAGFASTLCTCTYPMELIKTRVTIEKDVDYDNVAHAFVKIL	300
		241

FIGURE 1B

SEQ ID NO:10	* * * * *	* * *	****
SEQ ID NO:18	KDGGVGAFAAGISPTLVGMLPYSTCFYFMYDTIKESYCRTKSKS---	LSRPEMLLIGAL	
SEQ ID NO:21	RDEGPGEIYRGLAPSLIGVVPYAAANFYAYETLRGVYRRASGK---	EEVGNVPTLLIGSA	
	RDEGPSELYRGLTPSLIGVVPYAAACNFYAYETLKRLYRRATGRRRPGADVGPVATLLIGSA		360
	301		
SEQ ID NO:10	* * * * *	* * *	****
SEQ ID NO:18	AGFTASTISFPLEVARKRLMVGALQKCP-PNMAAALSEVIREEGLKGLYRGWGASCLKV		
SEQ ID NO:21	AGAIASTATFPLEVARKQMVGAVGGRQVYKNVLHAMYCILEKEGTAGLYRGLGPPSCIKL		
	AGAIASSATFPLEVARKQMVGAVGGRQVYQNVLHAIYCILKKEGAGGLYRGLGPPSCIKL		420
	361		
SEQ ID NO:10	* * * * *	* * *	****
SEQ ID NO:18	MPSSGITWMFYEAWKDILLVQ-----	NGNPL	
SEQ ID NO:21	MPAAGISFMCYEACKKILVDEKEDGGAAEPQEEETETGQAGGQAAPKSSNGDRP		
	MPAAGIAFMCYEACKKILVDKEDE-----	EEDEAG--GGEDDKKKVE----	473
	421		